fig-1

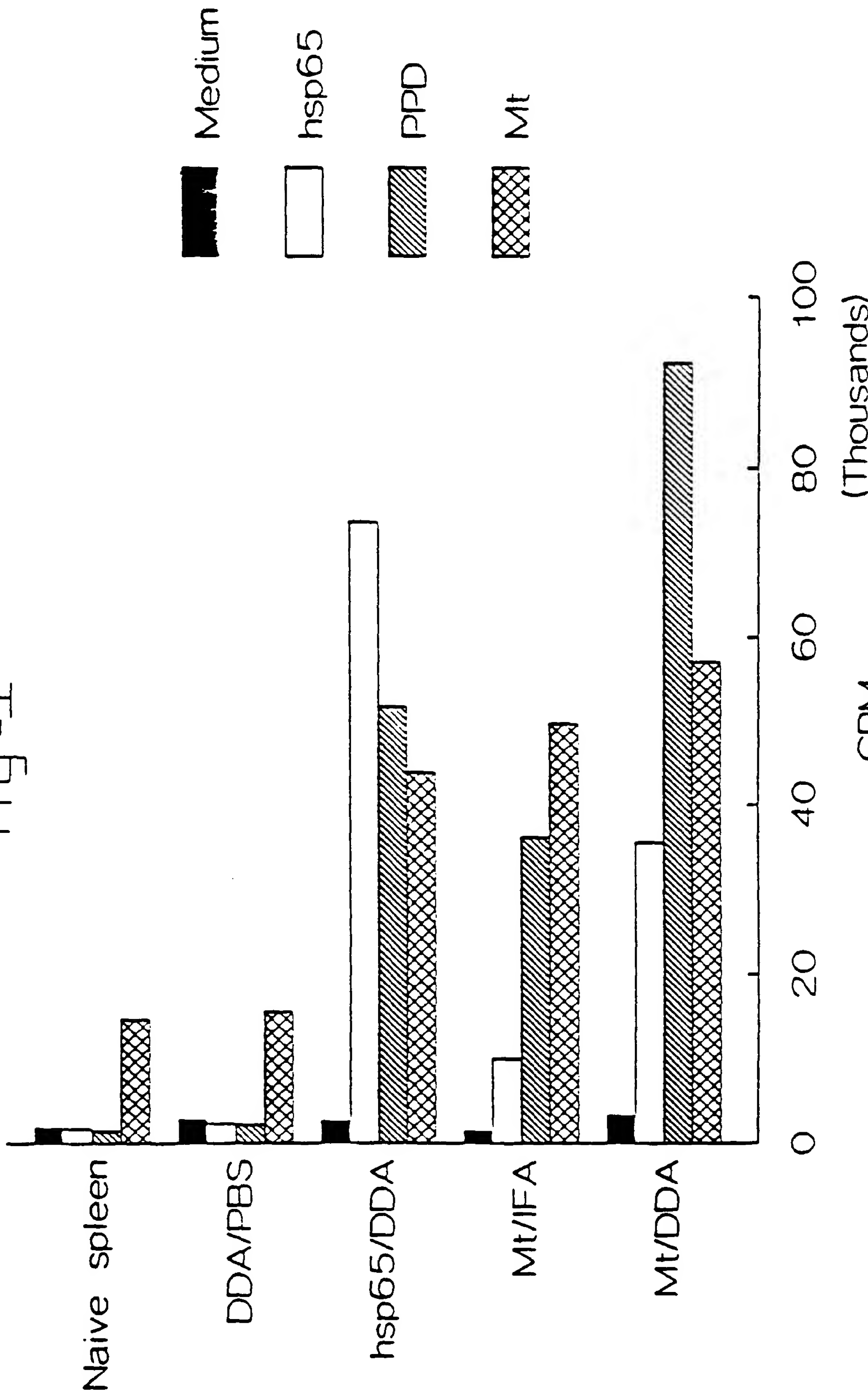
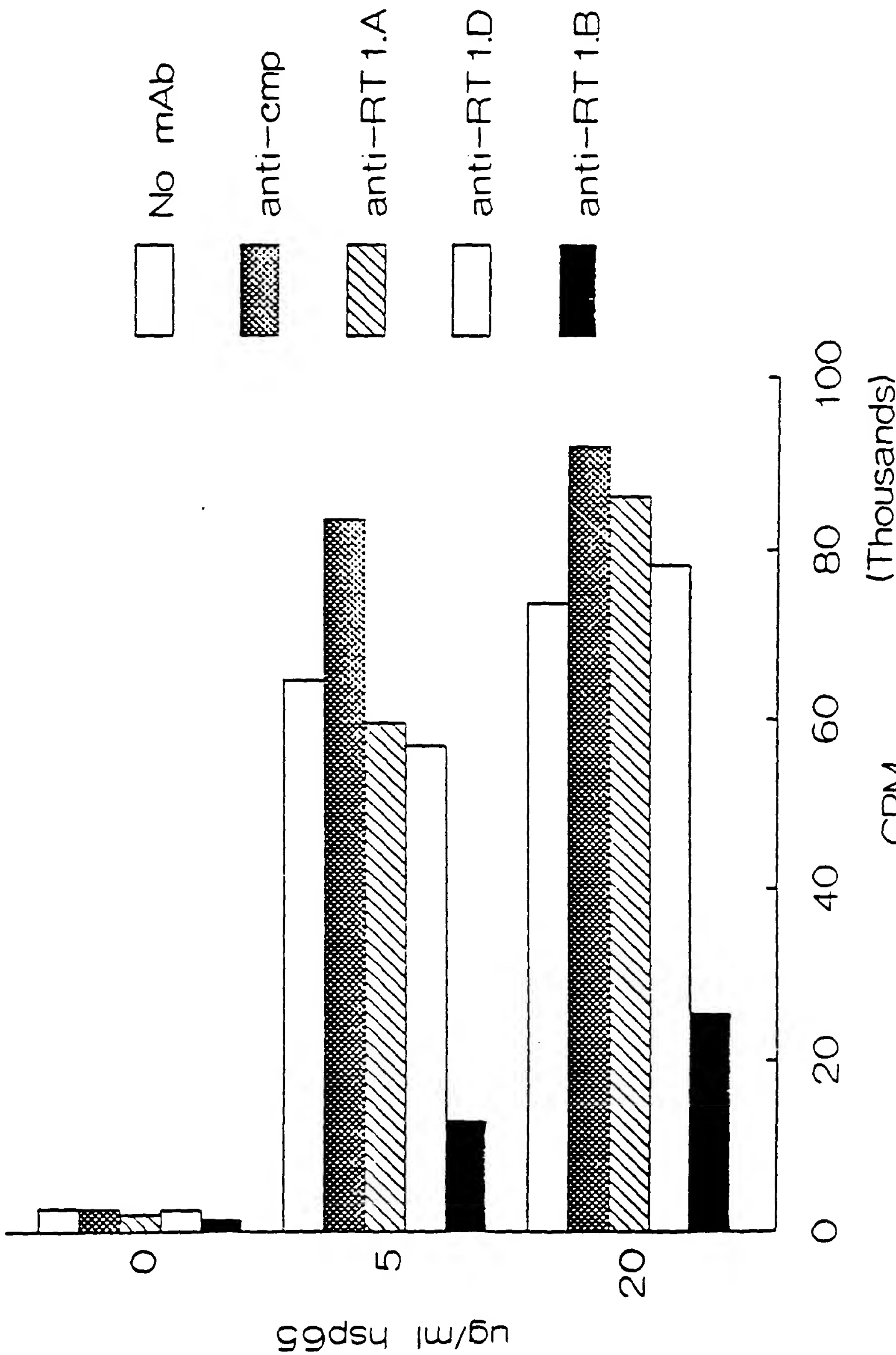

Medium
hsp65
PPD
Mt
Naive spleen
DDA/PBS
hsp65/DDA
Mt/IFA
Mt/DDA
0
20
40
60
80
100
CPM
(Thousands)

fig-2


No mAb
anti-cmp
anti-RT1.A
anti-RT1.D
anti-RT1.B
0
20
40
60
80
100
CPM (Thousands)
0
5
20
ug/ml hsp65

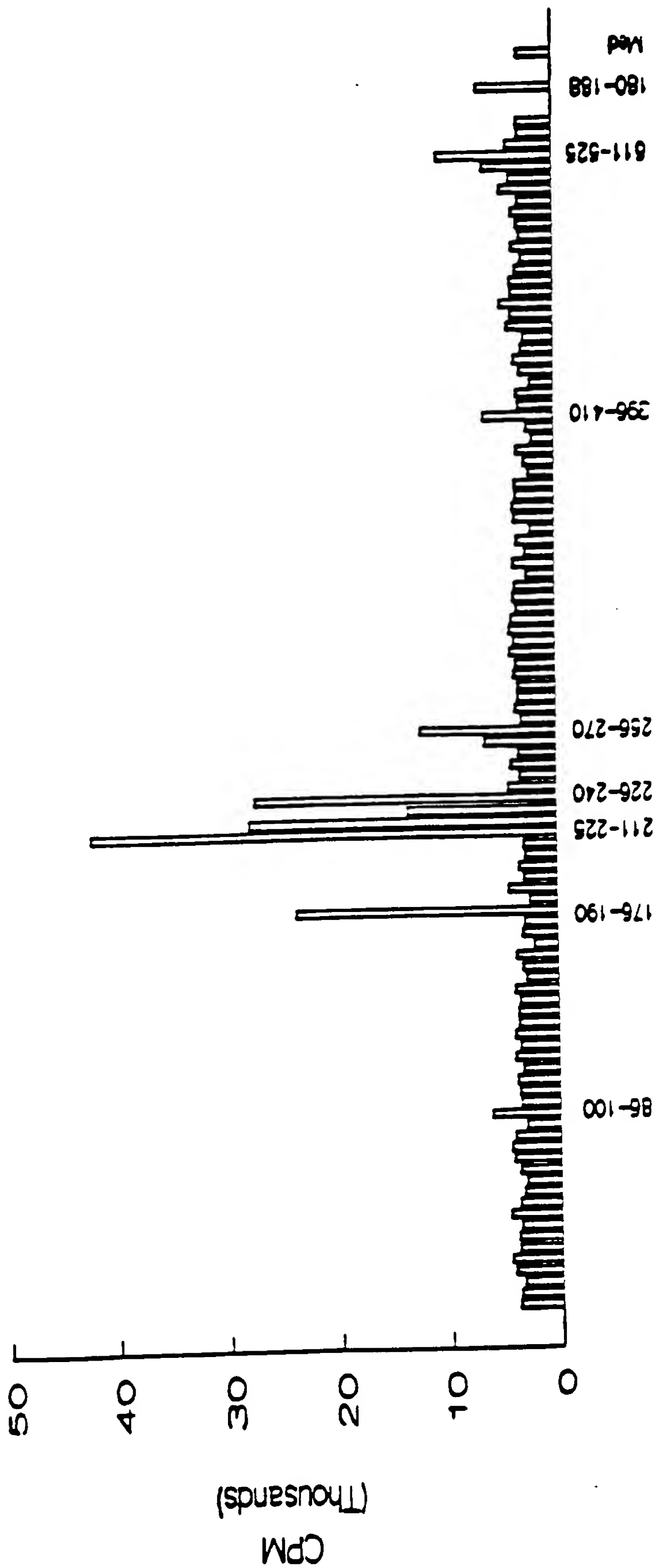

Med
180-188
396-410
256-270
226-240
211-225
176-190
86-100
0
10
20
30
40
50
CPM
(Thousands)

Fig-3a

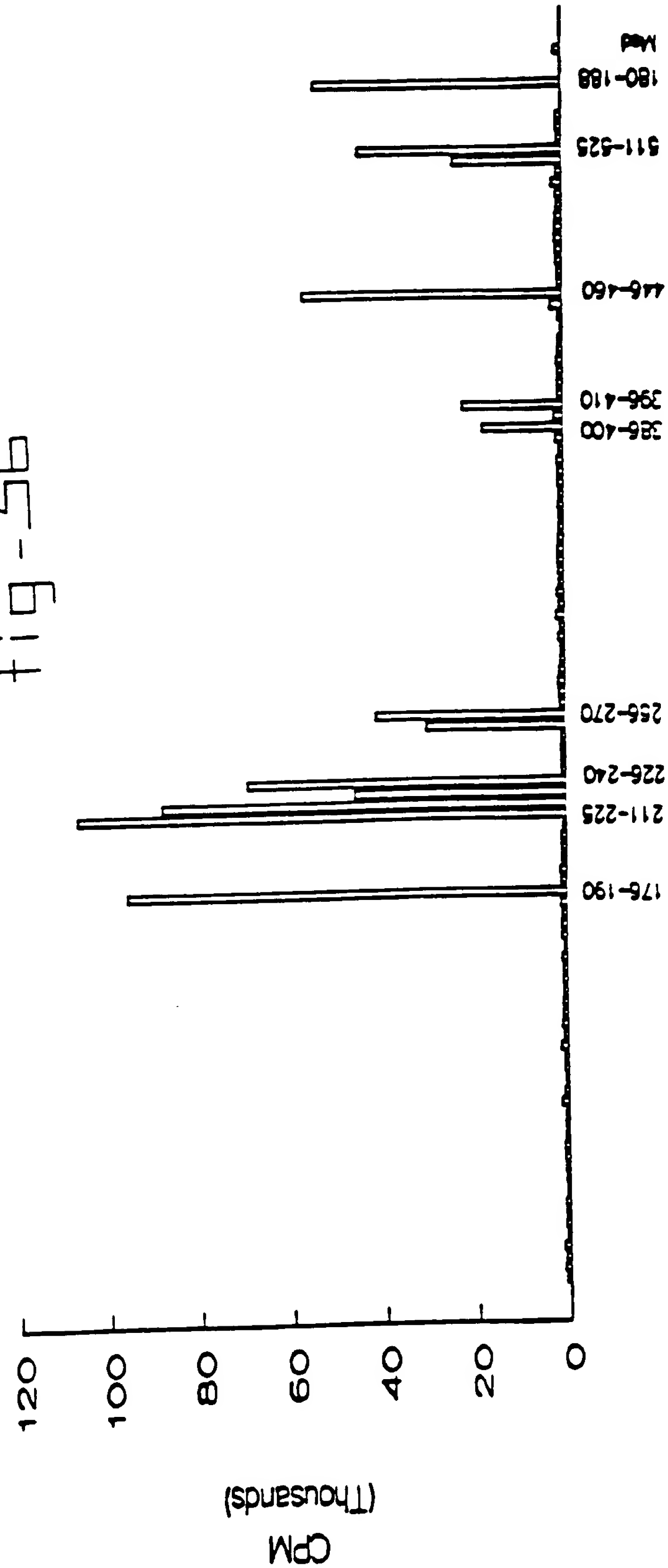

Med
180-188
511-525
446-460
396-410
386-400
256-270
226-240
211-225
176-190
0
20
40
60
80
100
120
CPM
(Thousands)

Fig-3b

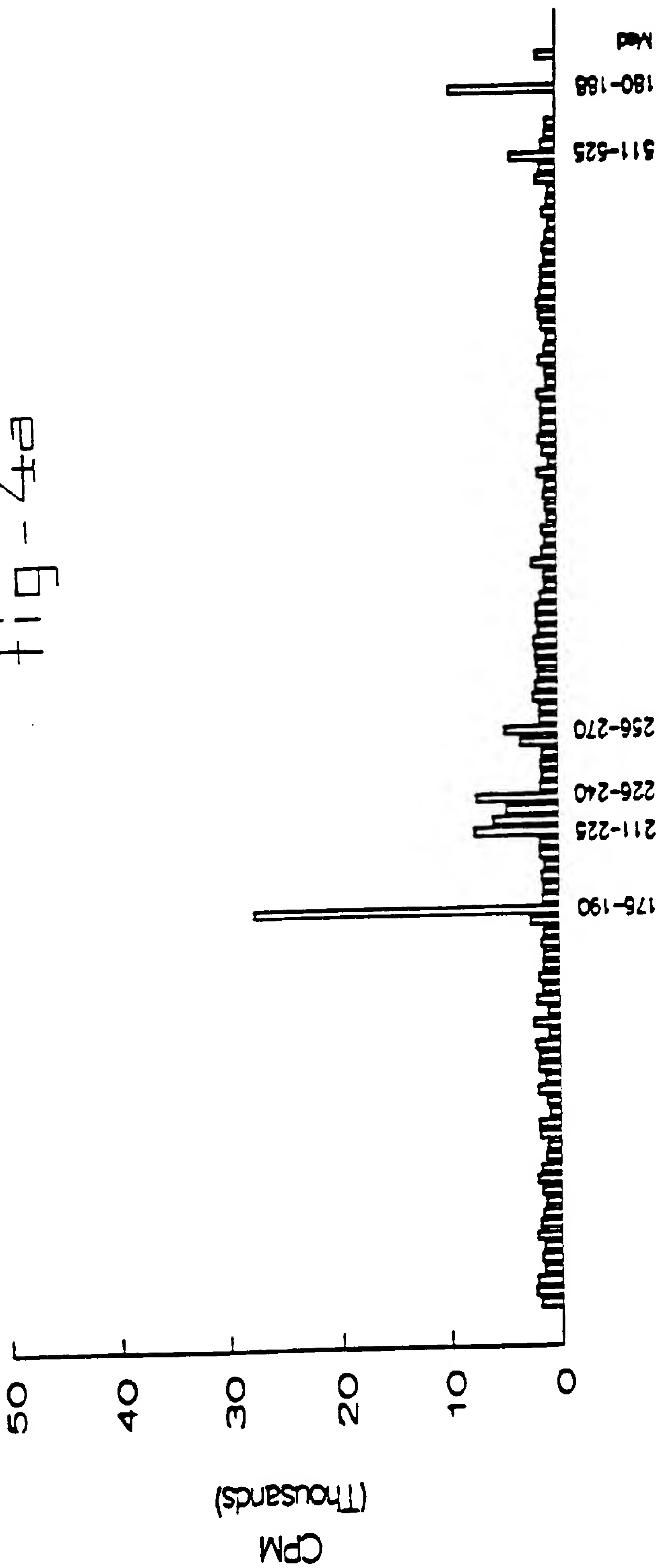

CPM
(Thousands)
0
10
20
30
40
50
176-190
211-225
226-240
256-270
511-525
180-188
Med

Fig-4a

08/716169

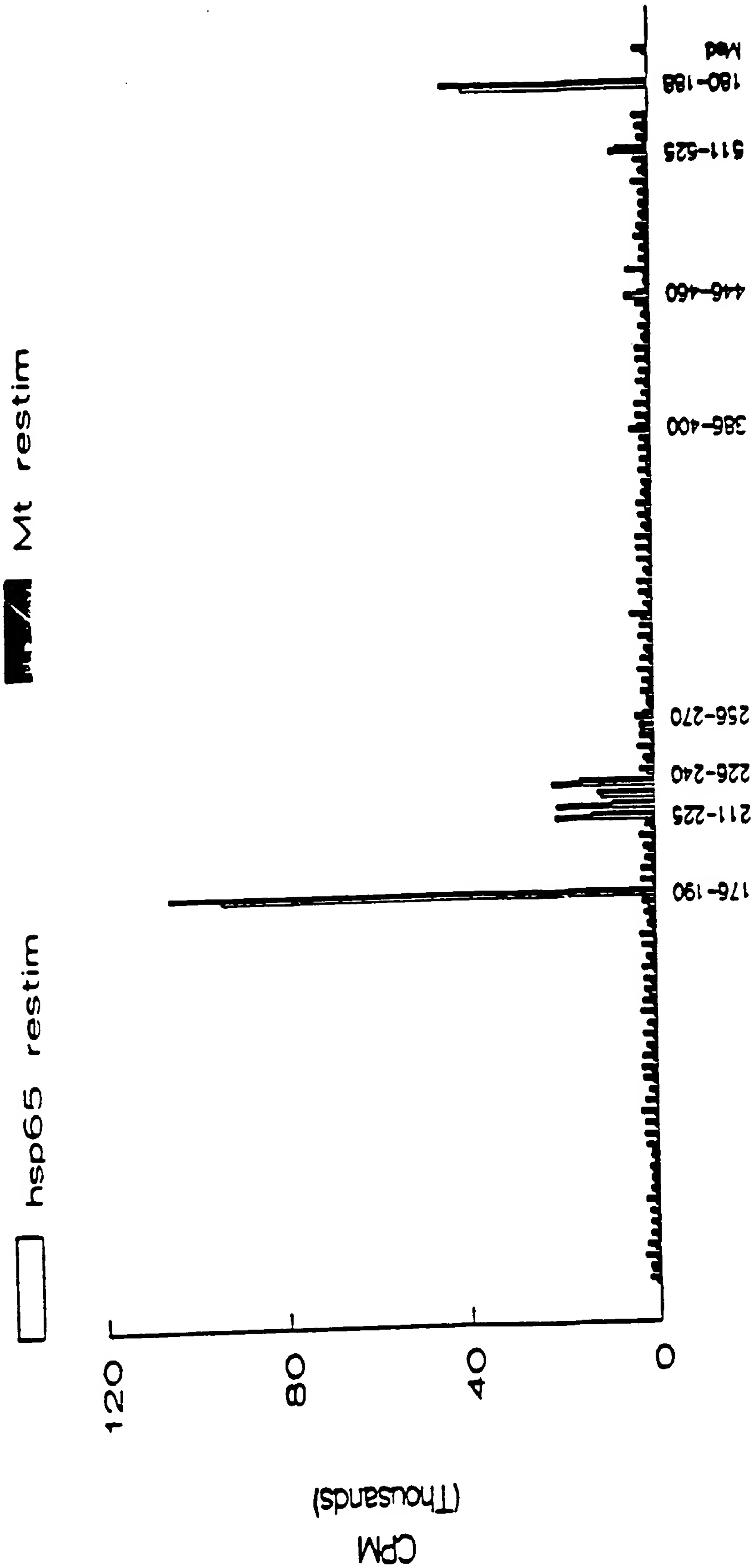


Fig - 4b

08/716169

Fig - 5.1

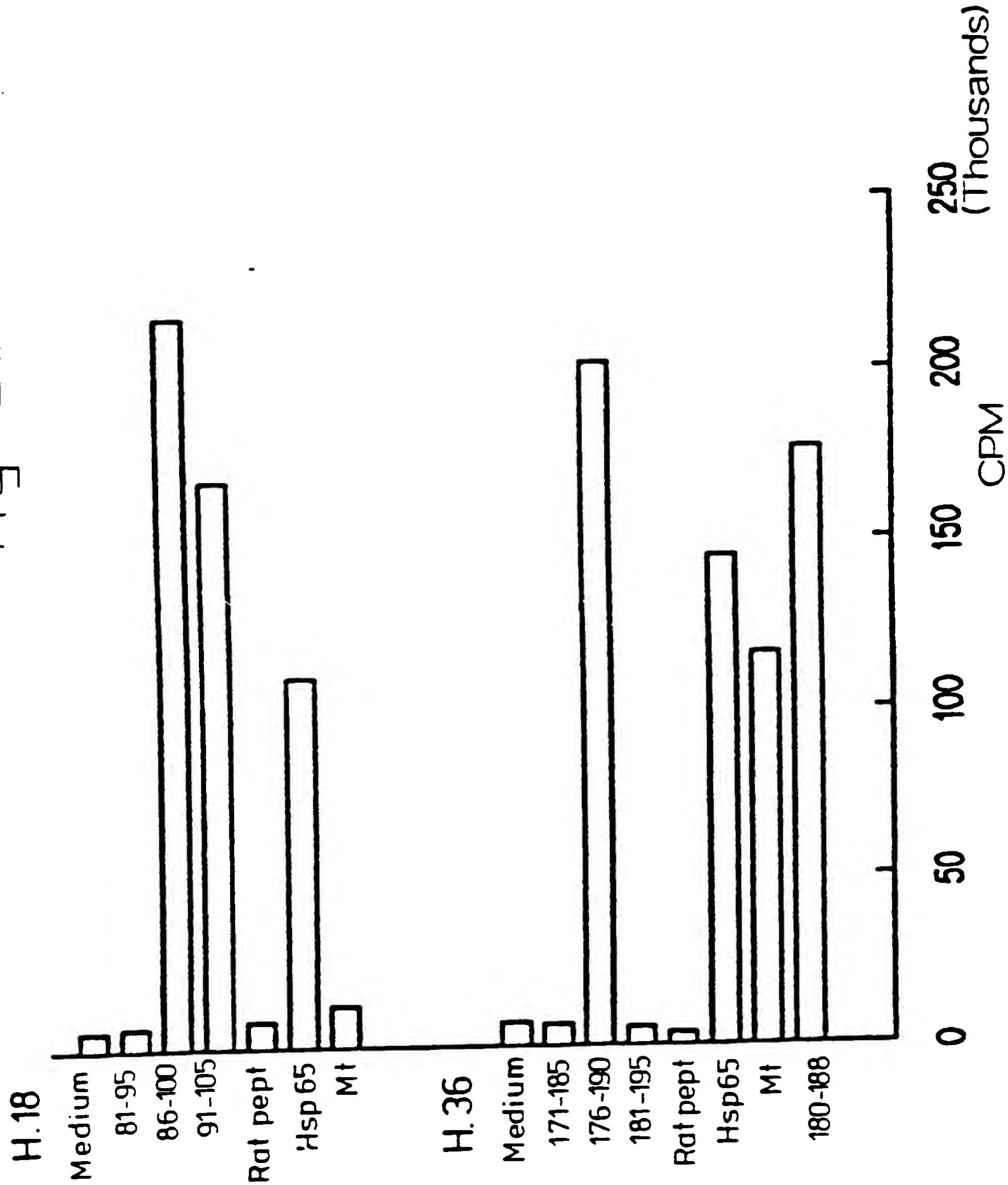
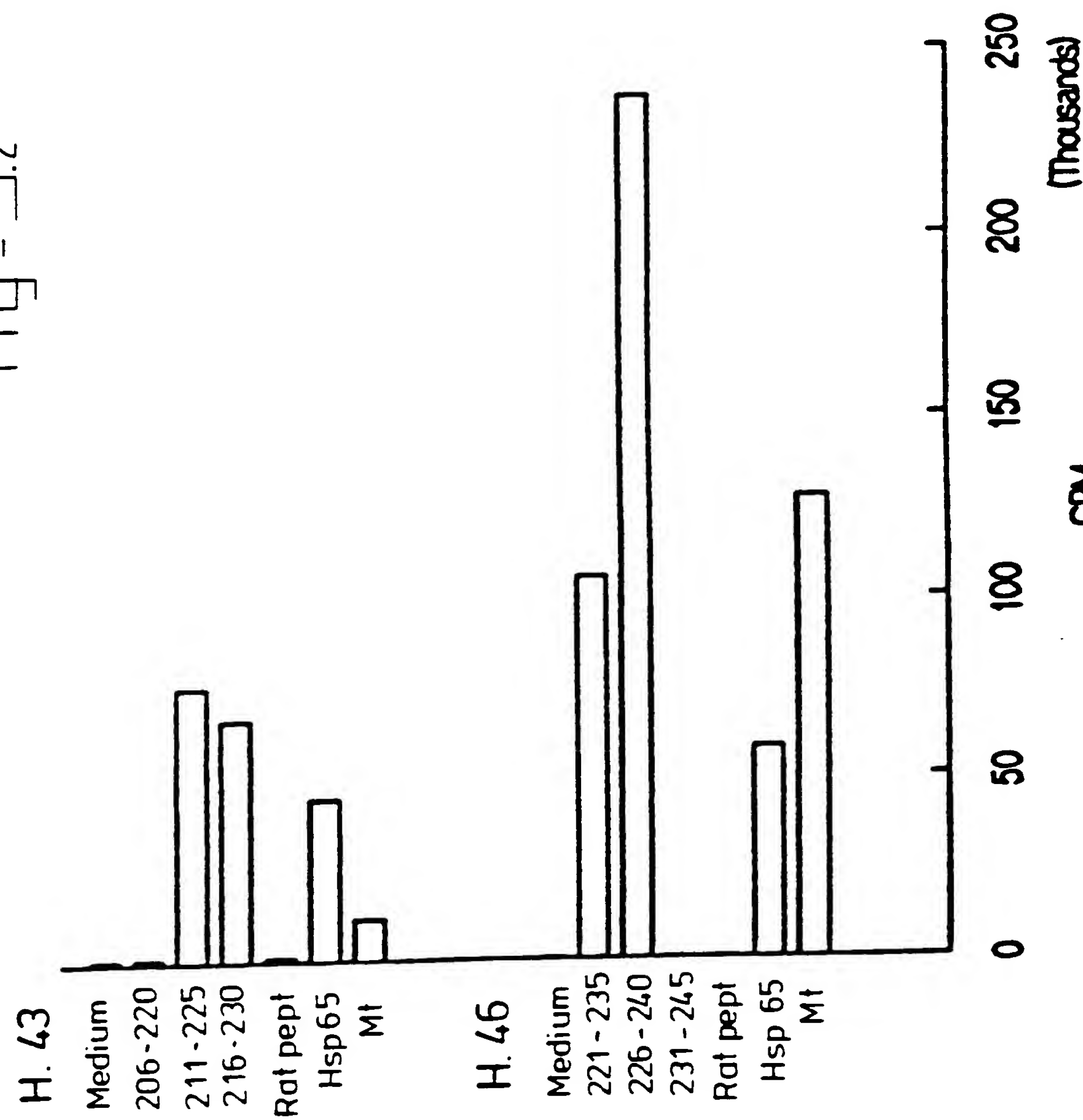


Fig-5.2


H. 43
Medium
206-220
211-225
216-230
Rat pept
Hsp65
Mt
H. 46
Medium
221-235
226-240
231-245
Rat pept
Hsp 65
Mt
0
50
100
150
200
250
CPM
(Thousands)

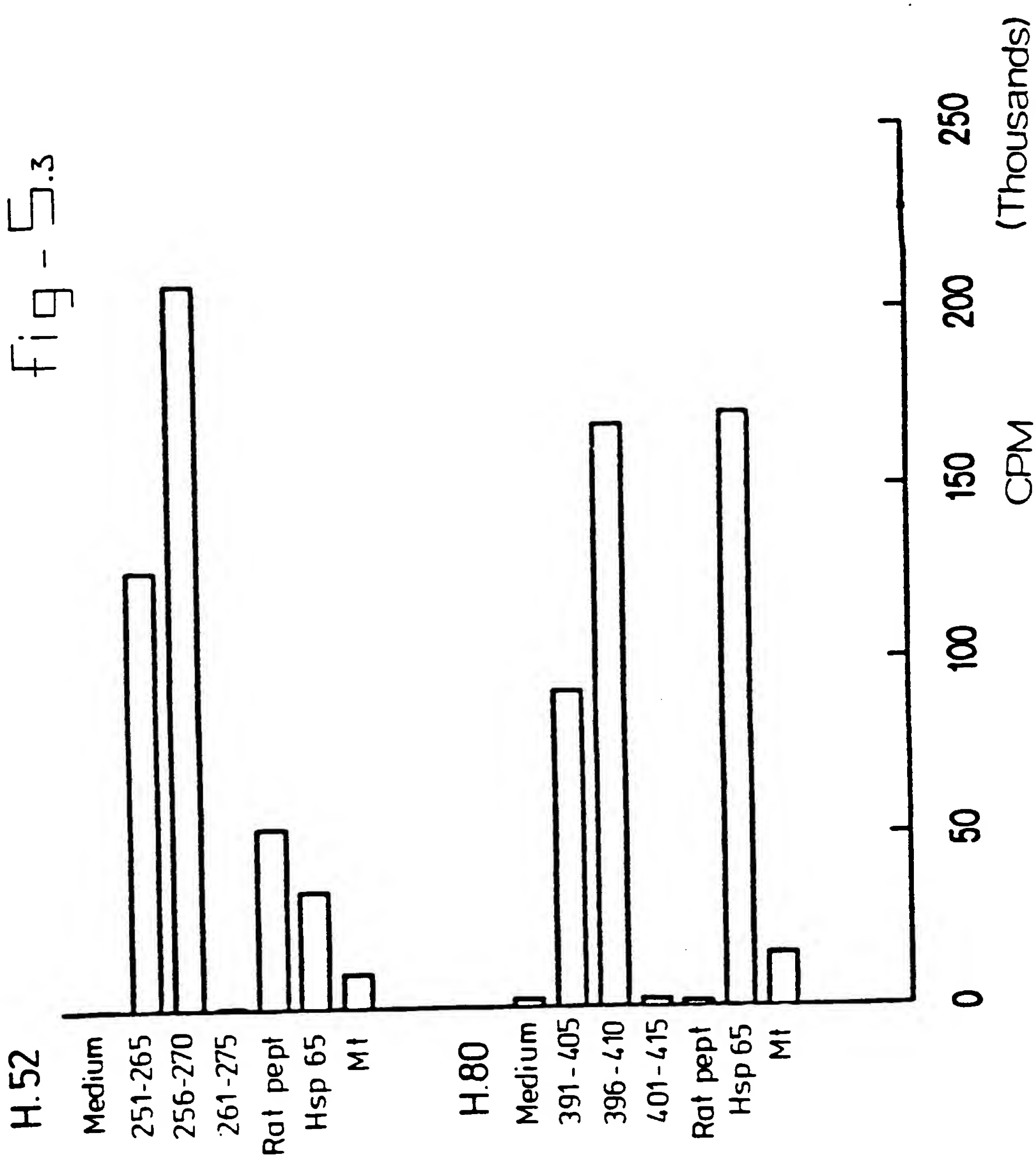
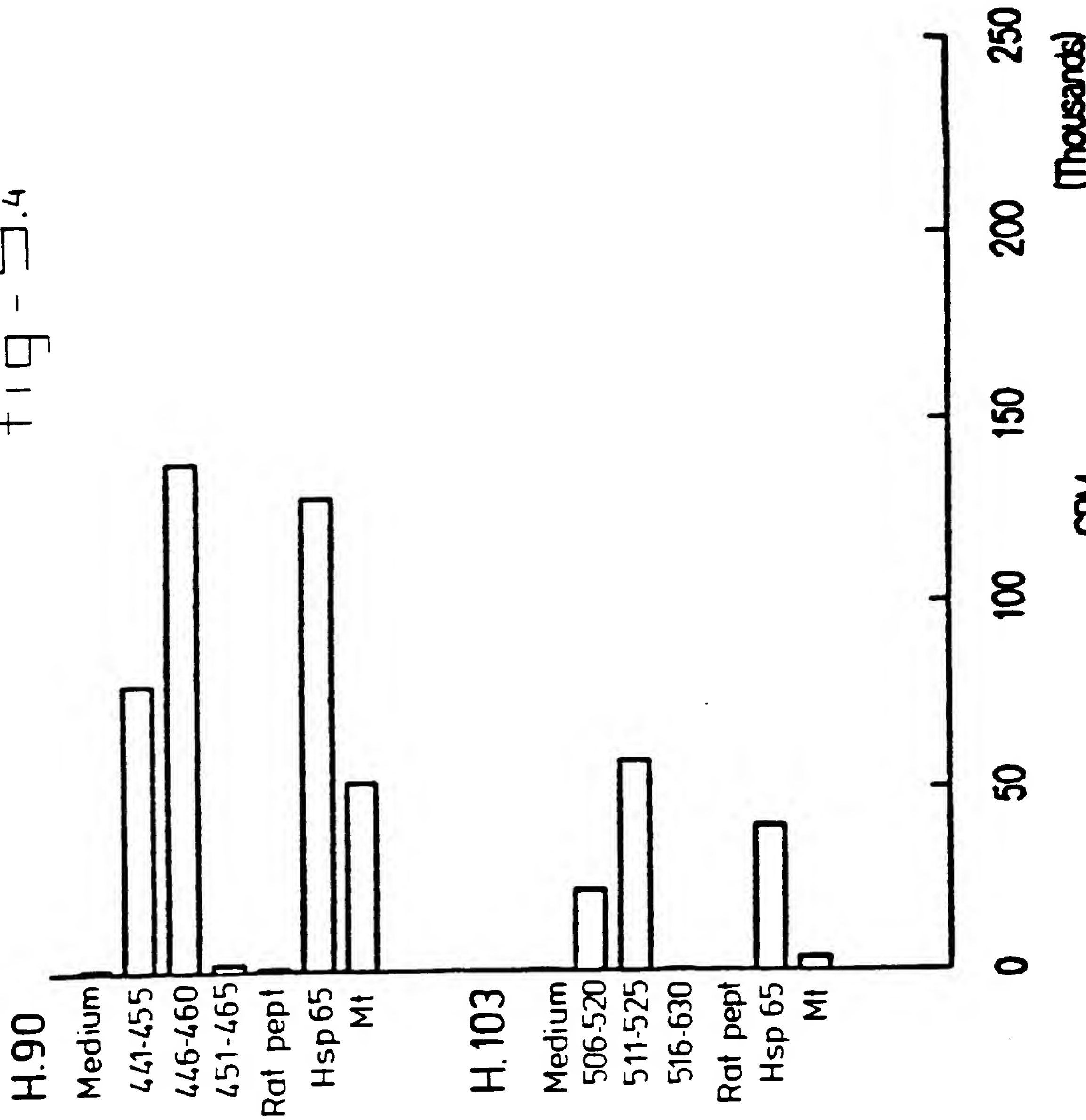

H.52
Medium
251-265
256-270
261-275
Rat pept
Hsp 65
Mt
H.80
Medium
391-405
396-410
401-415
Rat pept
Hsp 65
Mt
0
50
100
150
200
250
CPM
(Thousands)

Fig - 3

08/716169
PCT/NL95/00108

Fig - 5.4



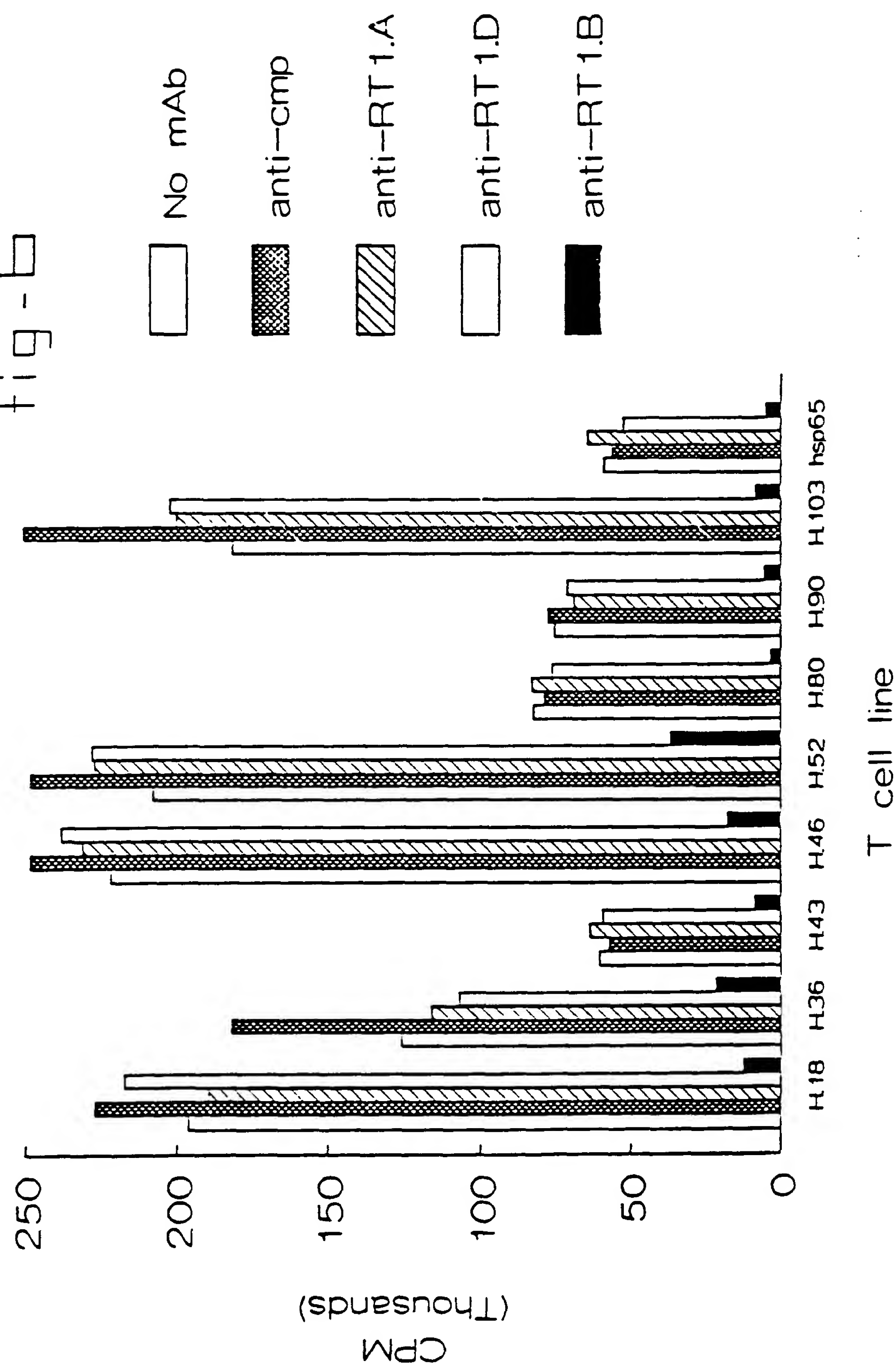

No mAb
anti-cmp
anti-RT1.A
anti-RT1.D
anti-RT1.B
CPM
(Thousands)
250
200
150
100
50
0
H18
H36
H43
H46
H52
H80
H90
H103
hsp65
T cell line

Fig-6

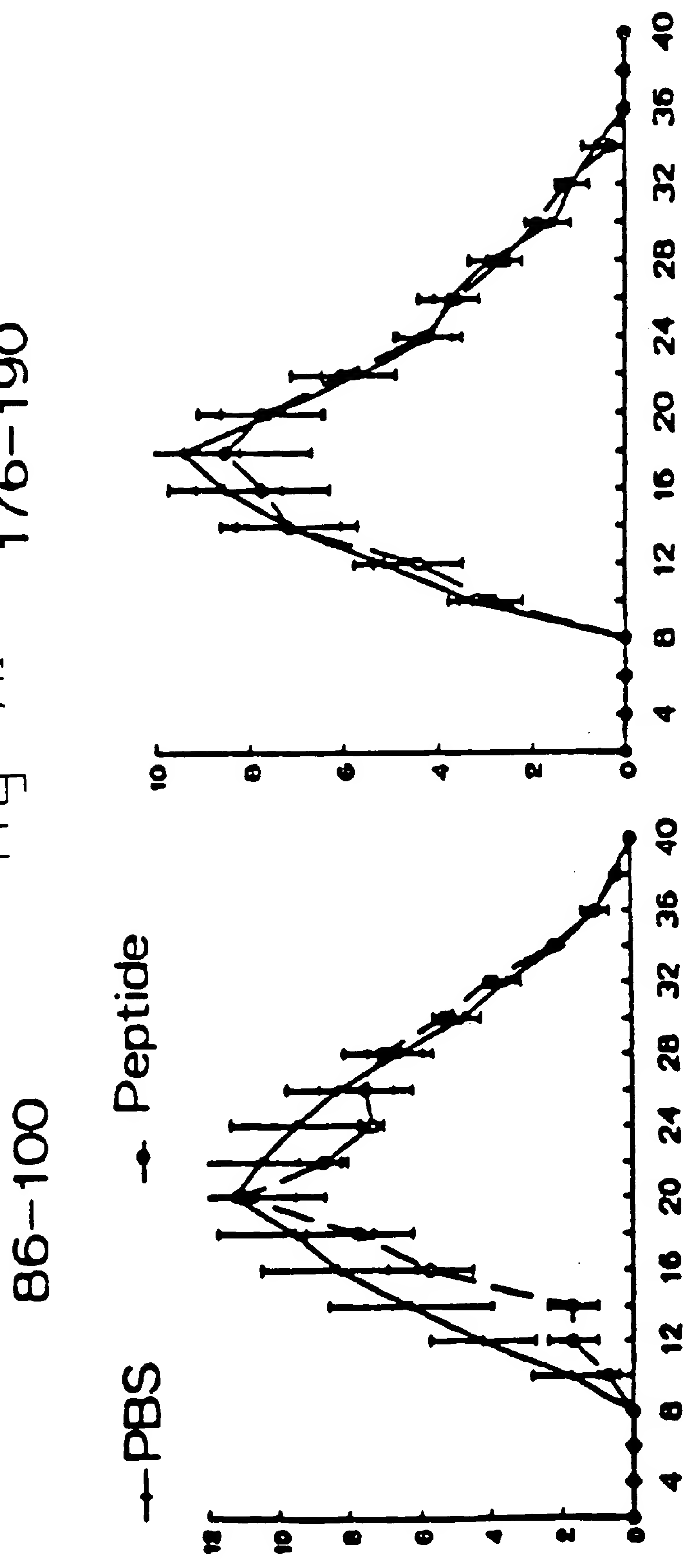


fig-7.1

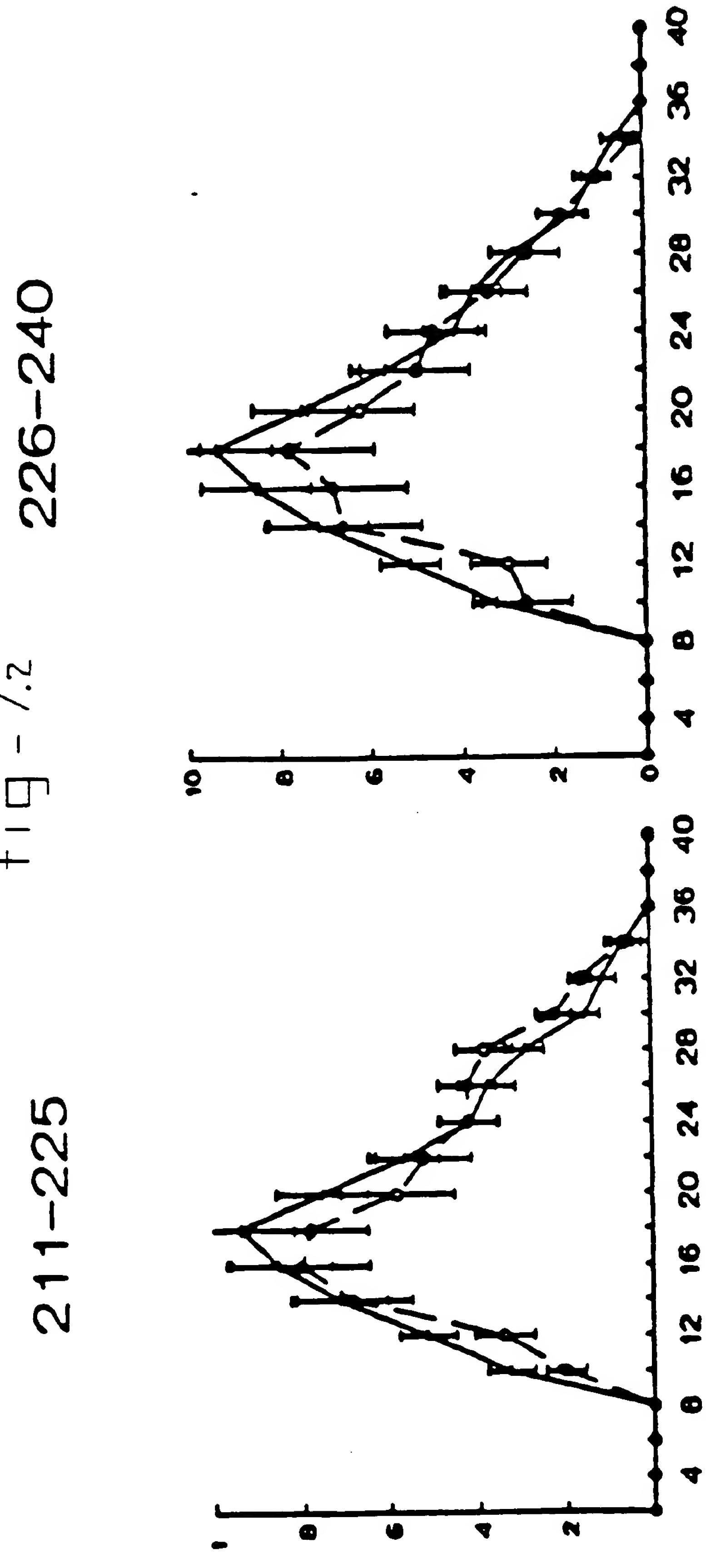


Fig - 7.2

08/716169

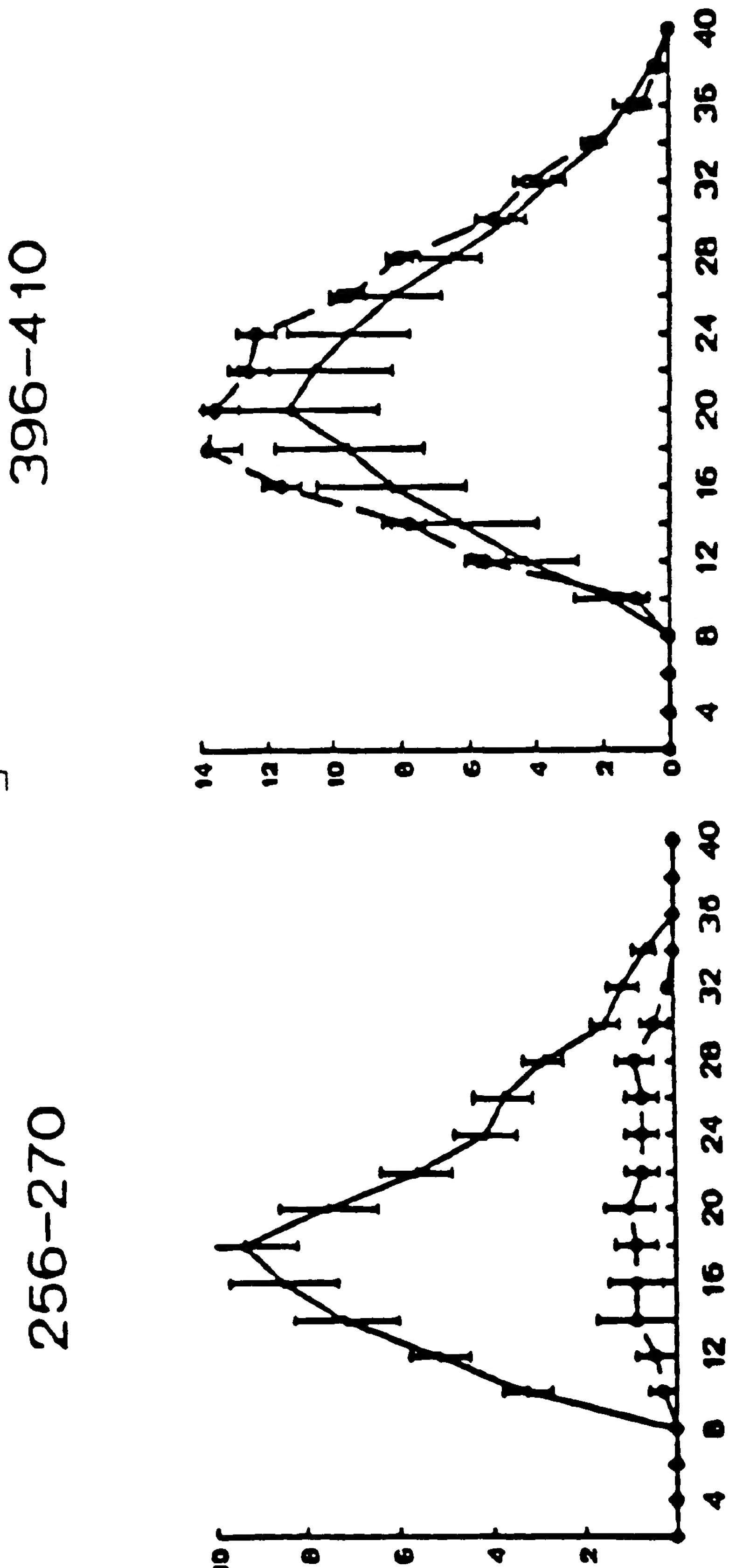


Fig - 7.3

Fig - 7.4

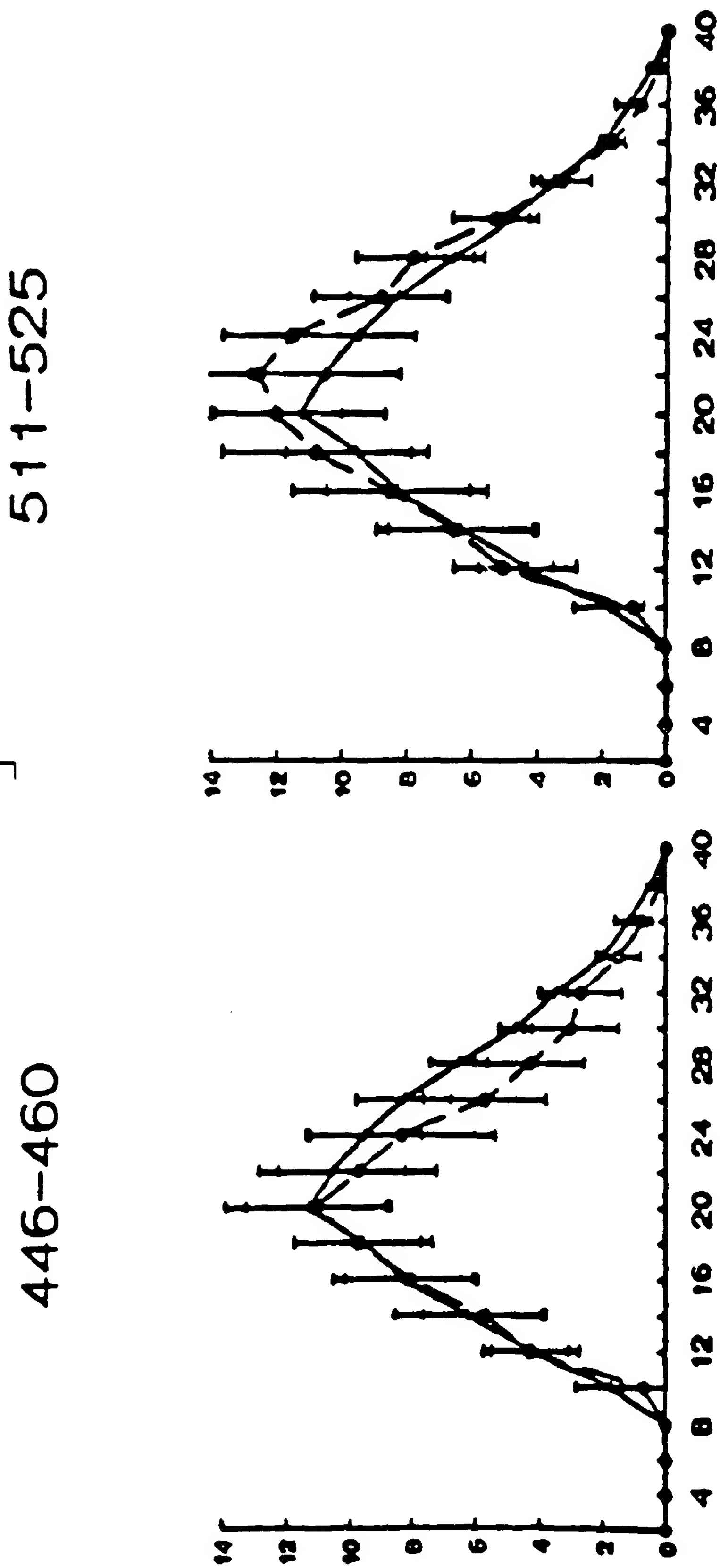


Fig - 8

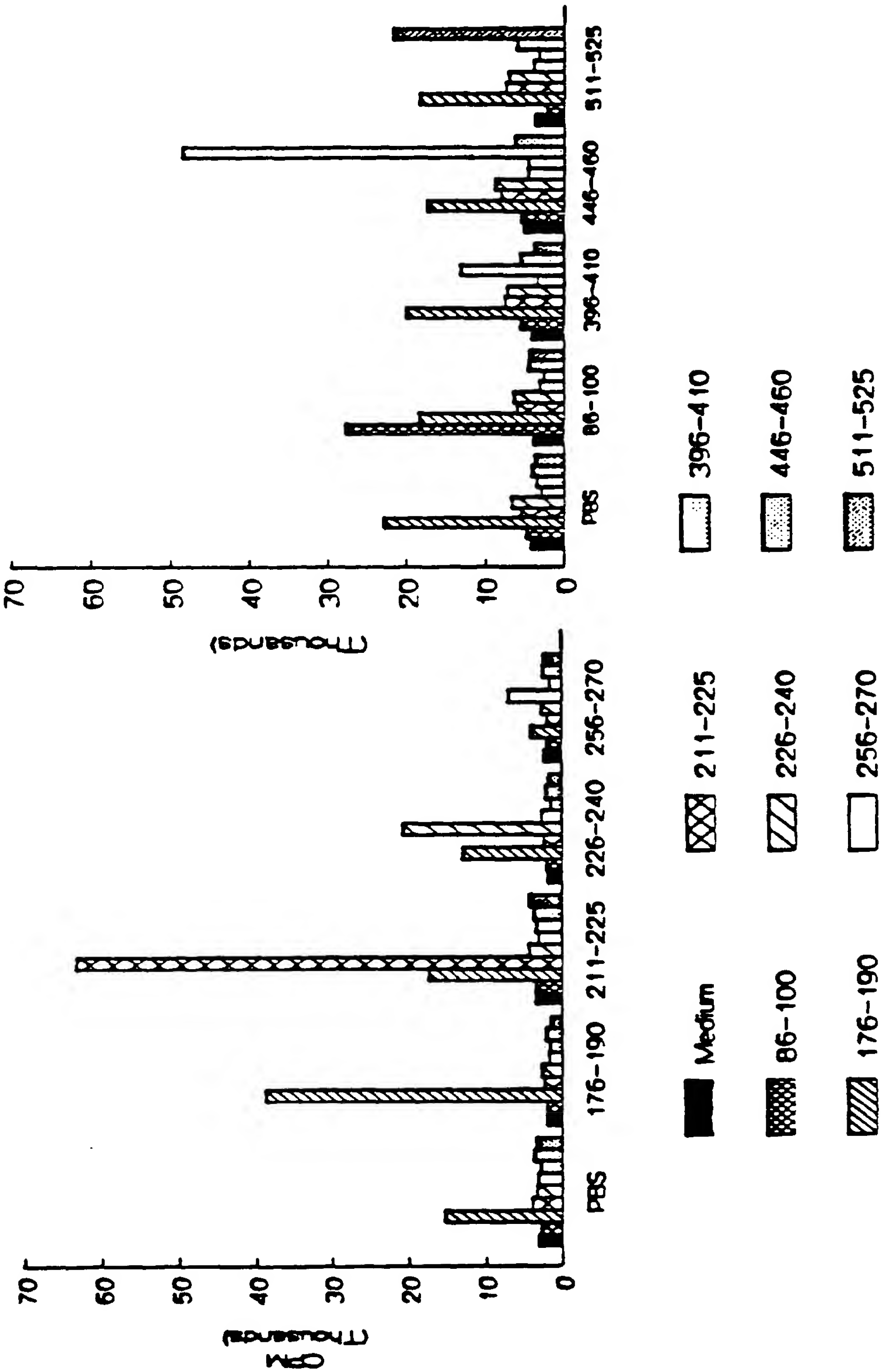

CPM
(Thousands)
0
10
20
30
40
50
60
70
PBS
176-190
211-225
226-240
256-270
(Thousands)
86-100
396-410
446-460
511-525
Medium
86-100
176-190
211-225
226-240
256-270
396-410
446-460
511-525

Fig - 9

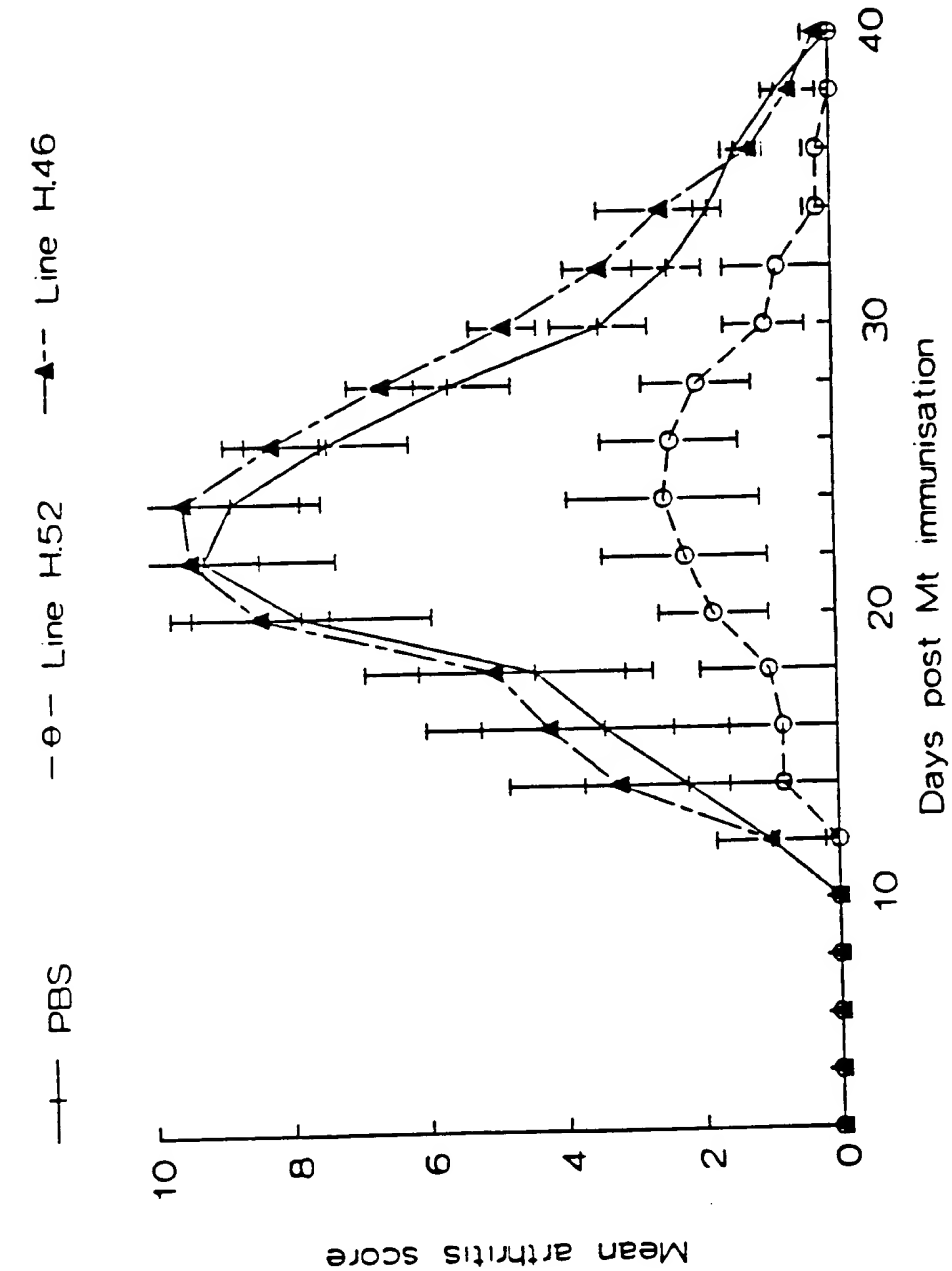

PBS
Line H.52
Line H.46
Mean arthritis score
0
2
4
6
8
10
Days post Mt immunisation
10
20
30
40

Fig-10

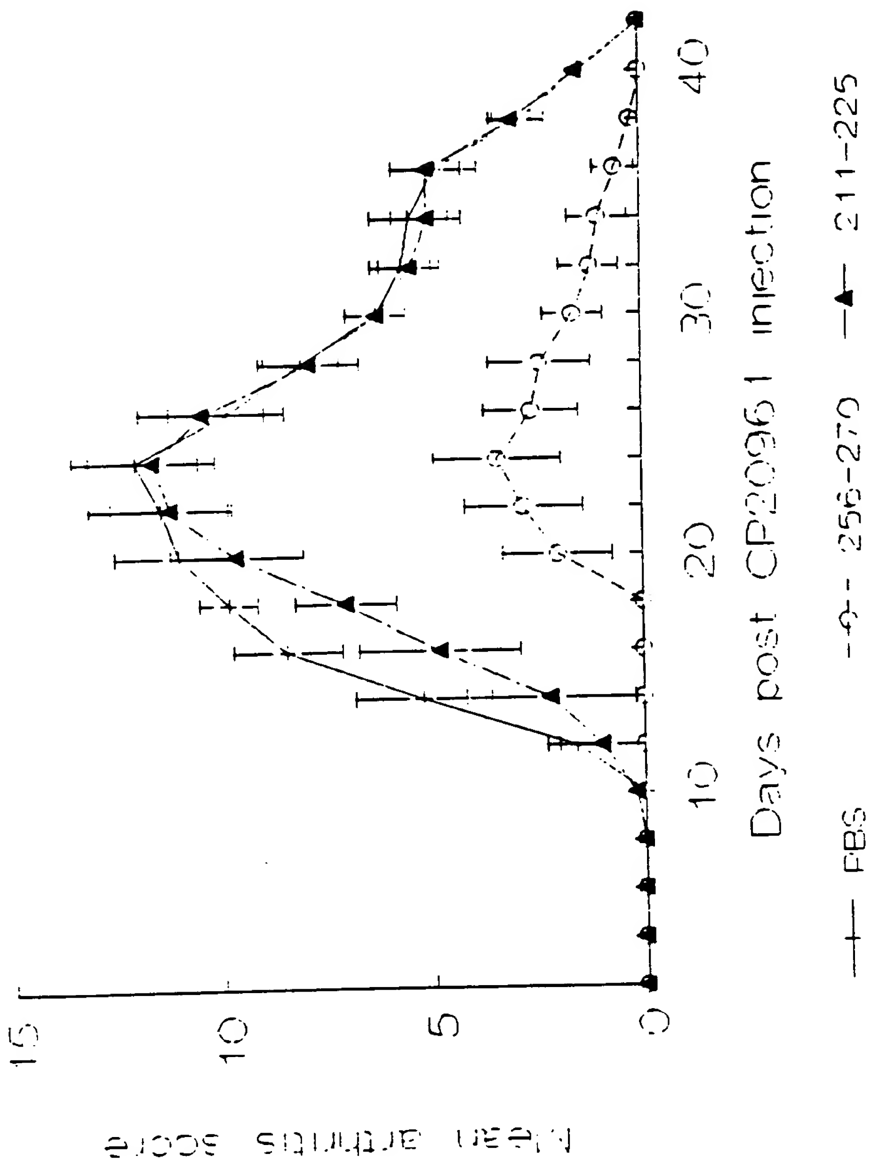

Mean arthritis score
0
5
10
15
10
20
30
40
Days post CP20961 injection
FBS
256-270
211-225

Fig 11

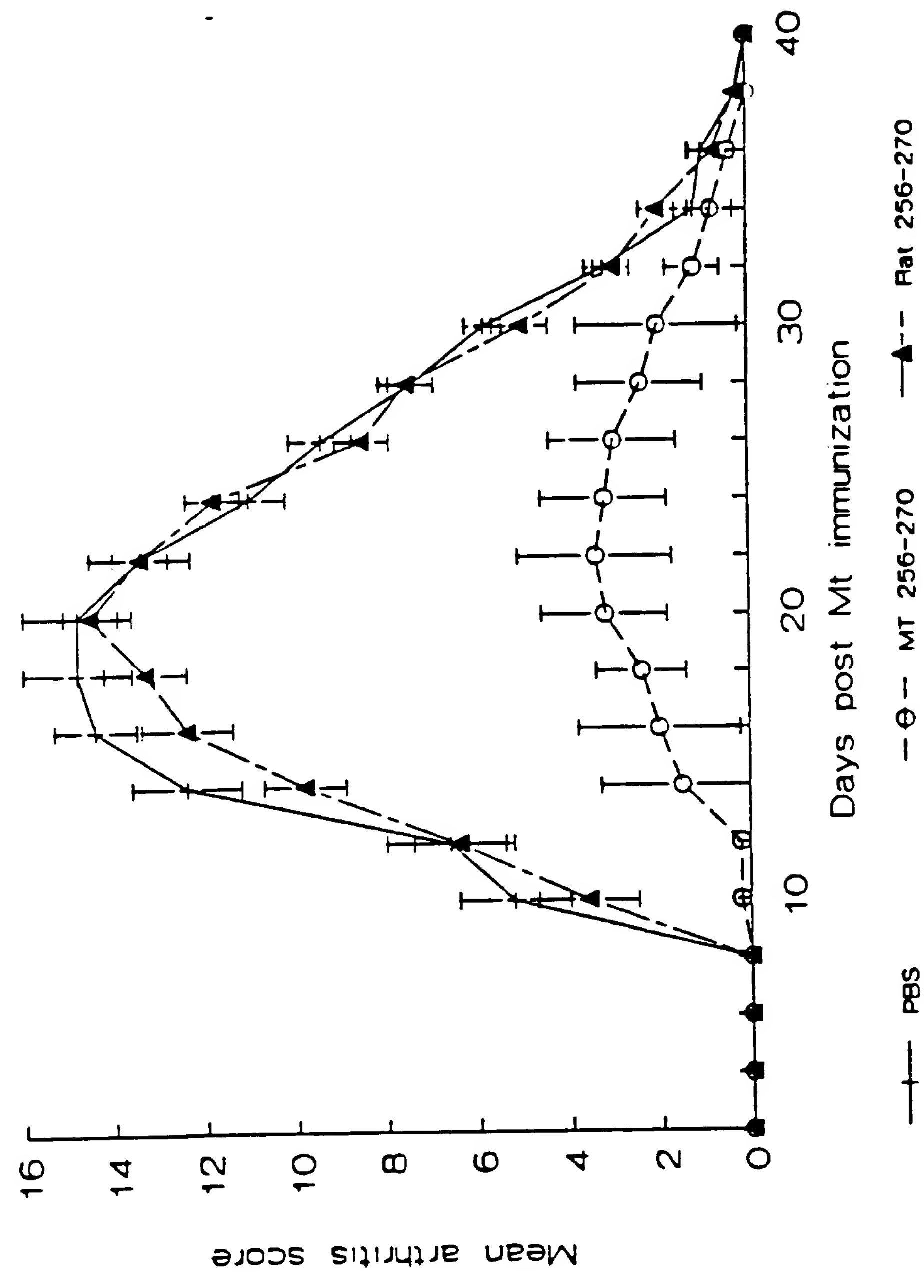
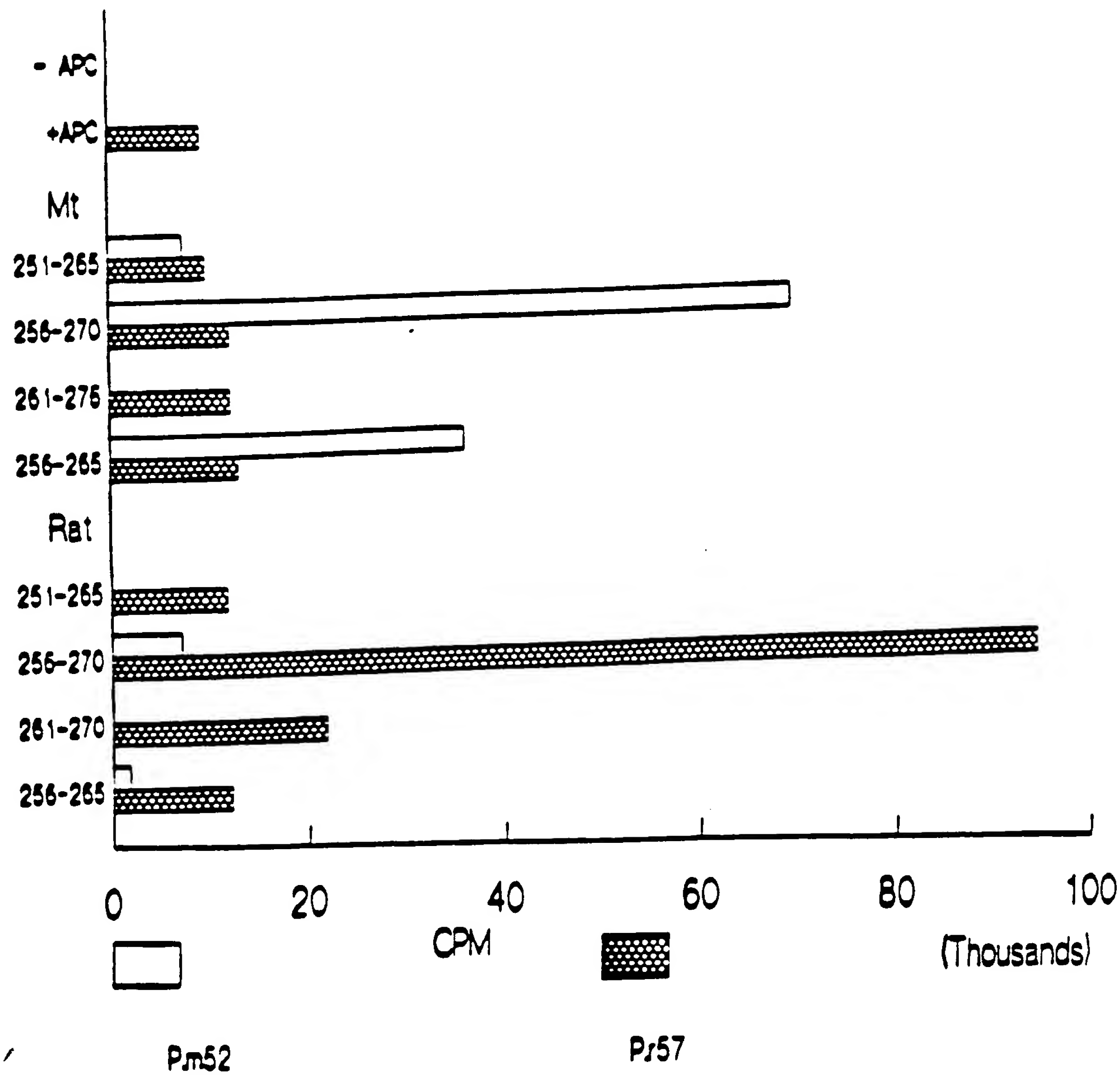

Mean arthritis score
0
2
4
6
8
10
12
14
16
10
20
30
40
Days post Mt immunization
PBS
MT 256-270
Rat 256-270

Fig-12


- APC
+APC
Mt
251-265
256-270
261-275
256-265
Rat
251-265
256-270
261-270
256-265
0
20
40
60
80
100
CPM
(Thousands)
Pm52
Pr57

08/716169

Fig. 13 (1)

```
*****************************************
* MULTIPLE SEQUENCE ALIGNMENT HSP60 *
*****************************************

HUMAN   MLRLPTVFRQMRPVSRVLAPHLTRAYAKDVKF    32
RAT     ------------------A--------KDVKF     6
MOUSE   ------------------APHLTRAYAKDVKF    14
M.TUB   M-------------------------AKTIAY     7
                                   *.. .

HUMAN   GADARALMLQGVDLLADAVAVTMGPKGRTVII    64
RAT     GADARALMLQGVDLLADAVAVTMGPKGRTVII    38
MOUSE   GADARALMLQGVDLLADAVAVTMGPKGRTVII    46
M.TUB   DEEARRGLERGLNALADAVKVTLGPKGRNVVL    39
        ...**  . .*.. ***** **.*****.*..

HUMAN   EQSWGSPKVTKDGVTVAKSIDLKDKYKNIGAK    96
RAT     EQSWGSPKVTKDGVTVAKSIDLKDKYKNIGAK    70
MOUSE   EQSWGSPKVTKDGVTVAKSIDLKDKYKNIGAK    78
M.TUB   EKKWGAPTITNDGVSIAKEIELEDPYEKIGAE    71
        *..**.*..*.***..**.*.*.* *..***.

HUMAN   LVQDVANNTNEEAGDGTTTATVLARSIAKEGF   128
RAT     LVQDVANNTNEEAGDGTTTATVLARSIAKEGF   102
MOUSE   LVQDVANNTNEEAGDGTTTATVLARSIAKEGF   110
M.TUB   LVKEVAKKTDDVAGDGTTTATVLAQALVREGL   103
        **..**..*.. ************.....**.

HUMAN   EKISKGANPVEIRRGVMLAVDAVIAELKKQSK   160
RAT     EKISKGANPVEIRRGVMLAVDAVIAELKKQSK   134
MOUSE   EKISKGANPVEIRRGVMLAVDAVIAELKKQSK   142
M.TUB   RNVAAGANPLGLKRGIEKAVEKVTETLLKGAK   135
         ... ****....**.  **. *...* * .*

HUMAN   PVTTPEEIAQVATISANGDKEIGNIISDAMKK   192
RAT     PVTTPEEIAQVATISANGDKDIGNIISDAMKK   166
MOUSE   PVTTPEEIAQVATISANGDKDIGNIISDAMKK   174
M.TUB   EVETKEQIAATAAISA-GDQSIGDLIAEAMDK   166
         *.* *.**..*.*** **..**..*..**.*

HUMAN   VGRKGVITVKDGKTLNDELEIIEGMKFDRGYI   224
RAT     VGRKGVITVKDGKTLNDELEIIEGMKFDRGYI   198
MOUSE   VGRKGVITVKDGKTLNDELEIIEGMKFDRGYI   206
M.TUB   VGNEGVITVEESNTFGLQLELTEGMRFDKGYI   198
        **..*****....*.. .**..***.**.***

HUMAN   SPYFINTSKGQKCEFQDAYVLLSEKKISSIQS   256
RAT     SPYFINTSKGQKCEFQDAYVLLSEKKISSVQS   230
MOUSE   SPYFINTSKGQKCEFQDAYVLLSEKKFSSVQS   238
M.TUB   SGYFVTDPERQEAVLEDPYILLVSSKVSTVKD   230
        * **..... *.  ..*.*.** ..* *....

HUMAN   IVPALEIANAHRKPLVIIAEDVDGEALSTLVL   288
RAT     IVPALEIANAHRKPLVIIAEDVDGEALSTLVL   262
MOUSE   IVPALEIANAHRKPLVIIAEDVDGEALSTLVL   270
M.TUB   LLPLLEKVIGAGKPLLIIAEDVEGEALSTLVV   262
        ..* **  . . ***.******.********.
```

Fig. 13 (2)

```
HUMAN    NRLKVGLQVVAVKAPGFGDNRKNQLKDMAIAT    320
RAT      NRLKVGLQVVAVKAPGFGDNRKNQLKDMAIAT    294
MOUSE    NRLKVGLQVVAVKAPGFGDNRKNQLKDMAIAT    302
M.TUB    NKIRGTFKSVAVKAPGFGDRRKAMLQDMAILT    294
         *... ... **********.**. *.**** *

HUMAN    GGAVFGEEGLTLNLEDVQPHDLGKVGEVIVTK    352
RAT      GGAVFGEEGLNLNLEDVQAHDLGKVGEVIVTK    326
MOUSE    GGAVFGEEGLNLNLEDVQAHDLGKVGEVIVTK    334
M.TUB    GGQVISEE-VGLTLENADLSLLGKARKVVVTK    325
         **.*..** ..*.**...   ***. .*.***

HUMAN    DDAMLLKGKGDKAQIEKRIQEIIEQLDVTTSE    384
RAT      DDAMLLKGKGDKAHIEKRIQEITEQLDITTSE    358
MOUSE    DDAMLLKGKGDKAHIEKRIQEITEQLDITTSE    366
M.TUB    DETTIVEGAGDTDAIAGRVAQIRQEIENSDSD    357
         *.. ...* **.. *. *...* .... ..*.

HUMAN    YEKEKLNERLAKLSDGVAVLKVGGTSDVEVNE    416
RAT      YEKEKLNERLAKLSDGVAVLKVGGTSDVEVNE    390
MOUSE    YEKEKLNERLAKLSDGVAVLKVGGTSDVEVNE    398
M.TUB    YDREKLQERLAKLAGGVAVIKAGAATEVELKE    389
         *..***.******..****.*.*....**..*

HUMAN    KKDRVTDALNATRAAVEEGIVLGGGCALLRCI    448
RAT      KKDRVTDALNATRAAVEEGIVLGGGCALLRCI    422
MOUSE    KKDRVTDALNATRAAVEEGIVLGGGCALLRCI    430
M.TUB    RKHRIEDAVRNAKAAVEEGIVAGGGVTLLQAA    421
         .*.*..**.....******** *** .**.

HUMAN    PALDSLTPANEDQKIGIEIIKRTLKIPAMTIA    480
RAT      PALDSLKPANEDQKIGIEIIKRALKIPAMTIA    454
MOUSE    PALDSLKPANEDQKIGIEIIKRALKIPAMTIA    462
M.TUB    PTLDELK-LEGDEATGANIVKVALEAPLKQIA    452
         *.**.*.  ..*. .* .*.* .*. * . **

HUMAN    KNAGVEGSLIVEKIMQSSSEVGYDAMAGDFVN    512
RAT      KNAGVEGSLIVEKILQSSSEVGYDAMLGDFVN    486
MOUSE    KNAGVEGSLIVEKILQSSSEVGYDAMLGDFVN    494
M.TUB    FNSGLEPGVVAEKVRNLPAGHGLNAQTGVYED    484
          *.*.* ....**. . ... * .*  * . .

HUMAN    MVEKGIIDPTKVVRTALLDAAGVASLLTTAEV    544
RAT      MVEKGIIDPTKVVRTALLDAAGVASLLTTAEA    518
MOUSE    MVEKGIIDPTKVVRTALLDAAGVASLLTTAEA    526
M.TUB    LLAAGVADPVKVTRSALQNAASIAGLFLTTEA    516
         ... *. **.**.*.** .**..*.*. *.*.

HUMAN    VVTEIPKEEKDPGMGAMGGMGGGMGGGMF    573
RAT      VVTEIPKEEKDPGMGAMGGMGGGMGGGMF    547
MOUSE    VVTEIPKEEKDPGMGAMGGMGGGMGGGMF    555
M.TUB    VVADKPEKEKASVPG-----GGDMGGMDF    540
         **.. *..**..  *     **.***  *

Consensus l ngth: 573
Identity (*)     : 254 ( 44.3%)
Similarity (.)   : 211 ( 36.8%)
```

08/716,169

Fig. 14 (1)

Glyceraldehyde-3-phosphate dehydrogenase sequences of
Bacillus stearothermophilus (upper sequence) and
Rattus norvegicus (Rat) (lower sequence)

+++ Identical aminoacids: Bacillus / Rat (182 = 54.3%)

\+ Similar, not identical aminoacids: Bacillus / Rat (115)

				5					10					15	
Ala	Val	Lys	Val	Gly	Ile	Asn	Gly	Phe	Gly	Arg	Ile	Gly	Arg	Asn	Val
	+++	+++	+++	+++	+	+++	+++	+++	+++	+++	+++	+++	+++		+++
-	Val	Lys	Val	Gly	Val	Asn	Gly	Phe	Gly	Arg	Ile	Gly	Arg	Leu	Val
					5					10					15

			20					25					30		
Phe	Arg	Ala	Ala	Leu	Lys	Asn	Pro	Asp	Ile	Glu	Val	Val	Ala	Val	Asn
	+++	+++	+++	+	+			+	+	+	+	+++	+++	+	+++
Thr	Arg	Ala	Ala	Phe	Ser	Cys	Asp	Lys	Val	Asp	Ile	Val	Ala	Ile	Asn
				20					25					30	

			35					40					45		
Asp	-	Leu	Thr	Asp	Ala	Asn	Thr	Leu	Ala	His	Leu	Leu	Lys	Tyr	Asp
+++		+	+	+++	+	+++		+	+	+	+	+	+	+++	+++
Asp	Pro	Phe	Ile	Asp	Leu	Asn	Tyr	Met	Val	Tyr	Met	Phe	Gln	Tyr	Asp
			35					40					45		

		50					55					60			
Ser	Val	His	Gly	Arg	Leu	Asp	Ala	Glu	Val	Ser	Val	Asn	Gly	Asn	Asn
+++	+	+++	+++	+	+	+	+	+	+++	+	+	+	+	+	+
Ser	Thr	His	Gly	Lys	Phe	Asn	Gly	Thr	Val	Lys	Ala	Glu	Asn	Gly	Lys
		50					55					60			

	65					70					75				
Leu	Val	Val	Asn	Gly	Lys	Glu	Ile	Ile	Val	Lys	Ala	Glu	Arg	Asp	Pro
+++	+++	+	+++	+++	+++		+++	+	+		+	+++	+++	+++	+++
Leu	Val	Ile	Asn	Gly	Lys	Pro	Ile	Thr	Ile	Phe	Gln	Glu	Arg	Asp	Pro
	65					70					75				

80					85					90					95
Glu	Asn	Leu	Ala	Trp	Gly	Glu	Ile	Gly	Val	Asp	Ile	Val	Val	Glu	Ser
	+	+		+++	+++	+		+++	+	+		+++	+++	+++	+++
Val	Lys	Ile	Lys	Trp	Gly	Asp	Ala	Gly	Ala	Glu	Tyr	Val	Val	Glu	Ser
80					85					90					95

				100					105					110	
Thr	Gly	Arg	Phe	Thr	Lys	Arg	Glu	Asp	Ala	Ala	Lys	His	Leu	Glu	Ala
+++	+++		+++	+++	+	+	+++	+	+++	+		+++	+++	+	+
Thr	Gly	Val	Phe	Thr	Thr	Met	Glu	Lys	Ala	Gly	Ala	His	Leu	Lys	Gly
				100					105					110	

08/716169

Fig. 14 (2)

```
            115                 120                 125
Gly Ala Lys Lys Val Ile Ile Ser Ala Pro Ala Lys Asn Glu Asp Ile
+++ +++ +++  +  +++ +++ +++ +++ +++ +++  +       +   +       +
Gly Ala Lys Arg Val Ile Ile Ser Ala Pro Ser Ala Asp Ala Pro Met
            115                 120                 125

        130                 135                 140
Thr Ile Val Met Gly Val Asn Gln Asp Lys Tyr Asp Pro Lys Ala His
     +  +++ +++ +++ +++ +++  +   +  +++ +++ +++      +   +
 -  Phe Val Met Gly Val Asn His Glu Lys Tyr Asp  -  Asn Ser Leu
            130                 135                     140

    145                 150                 155
His Val Ile Ser Asn Ala Ser Cys Thr Thr Asn Cys Leu Ala Pro Phe
 +   +   +  +++ +++ +++ +++ +++ +++ +++ +++ +++ +++ +++ +++  +
Lys Ile Val Ser Asn Ala Ser Cys Thr Thr Asn Cys Leu Ala Pro Leu
            145                 150                 155

160                 165                 170                 175
Ala Lys Val Leu His Glu Gln Phe Gly Ile Val Arg Gly Met Met Thr
+++ +++ +++  +  +++  +   +  +++ +++ +++ +++     +++  +  +++ +++
Ala Lys Val Ile His Asp Asn Phe Gly Ile Val Glu Gly Leu Met Thr
        160                165                 170

                180                 185                 190
Thr Val His Ser Tyr Thr Asn Asp Gln Arg Ile Leu Asp Leu Pro His
+++ +++ +++  +      +++  +   +  +++  +   +   +  +++     +++
Thr Val His Ala Ile Thr Ala Thr Gln Lys Thr Val Asp Gly Pro Ser
    175                 180                 185

            195                     200                 205
Lys Asp Leu Arg Arg  -  Ala Arg Ala Ala Ala Glu Ser Ile Ile Pro
     +  +++  +  +++      +  +++  +  +++ +++  +   +  +++ +++ +++
Gly Lys Leu Trp Arg Asp Gly Arg Gly Ala Ala Gln Asn Ile Ile Pro
190                 195                 200                 205

            210                 215                 220
Thr Thr Thr Gly Ala Ala Lys Ala Val Ala Leu Val Leu Pro Glu Leu
 +   +  +++ +++ +++ +++ +++ +++ +++  +      +++  +  +++ +++ +++
Ala Ser Thr Gly Ala Ala Lys Ala Val Gly Lys Val Ile Pro Glu Leu
                210                 215                 220

        225                 230                 235
Lys Gly Lys Leu Asn Gly Met Ala Met Arg Val Pro Thr Pro Asn Val
 +  +++ +++ +++  +  +++ +++ +++  +  +++ +++ +++ +++ +++ +++ +++
Asn Gly Lys Leu Thr Gly Met Ala Phe Arg Val Pro Thr Pro Asn Val
            225                 230                 235

    240                 245                 250
Ser Val Val Asp Leu Val Ala Glu Leu Glu Lys Glu Val Thr Val Glu
+++ +++ +++ +++ +++  +          +++ +++ +++      +   +       +
Ser Val Val Asp Leu Thr Cys Arg Leu Glu Lys Pro Ala Lys Tyr Asp
        240                 245                 250
```

08/716,169

Fig. 14 (3)

```
255                 260                 265                 270
Glu Val Asn Ala Ala Leu Lys Ala Ala Ala Glu Gly Glu Leu Lys Gly
 +   +   +       +   +  +++  +  +++ +++ +++ +++     +++ +++ +++
Asp Ile Lys Lys Val Val Lys Gln Ala Ala Glu Gly Pro Leu Lys Gly
    255                 260                 265

                275                 280                 285
Ile Leu Ala Tyr Ser Glu Glu Pro Leu Val Ser Arg Asp Tyr Asn Gly
+++ +++  +  +++  +  +++  +   +   +  +++ +++     +++  +  +++  +
Ile Leu Gly Tyr Thr Glu Asp Gln Val Val Ser Cys Asp Phe Asn Ser
270                 275                 280                 285

            290                 295                 300
Ser Thr Val Ser Ser Thr Ile Asp Ala Leu Ser Thr Met Val Ile Asp
 +   +      +++ +++ +++  +  +++ +++      +   +   +   +   +   +
Asn Ser His Ser Ser Thr Phe Asp Ala Gly Ala Gly Ile Ala Leu Asn
                290                 295                 300

        305                 310                 315
Gly Lys Met Val Lys Val Val Ser Trp Tyr Asp Asn Glu Thr Gly Tyr
 +   +   +  +++ +++  +   +  +++ +++ +++ +++ +++ +++     +++ +++
Asp Asn Ile Val Lys Leu Ile Ser Trp Tyr Asp Asn Glu Tyr Gly Tyr
            305                 310                 315

    320                 325             330
Ser His Arg Val Val Asp Leu Ala Ala Tyr Ile Ala Ser Lys Gly
+++  +  +++ +++ +++ +++ +++     +++ +++  +  +++ +++ +++  +
Ser Asn Arg Val Val Asp Leu Met Ala Tyr Met Ala Ser Lys Glu
        320                 325                 330
```